

# FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT  
GTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTCTTACACAGTG  
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA  
CTACTCTCTTCGACAGTCTTAGACTGGTCTTCTACACTAAGACACCAATGAAGGAGTATGTG  
CTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT  
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
ATGATGATGATGAGGACAACCTCTCTTTTTTCCAACAAGAGAGCCAAAGAAGCCATTTTTTTCCA  
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTCACGAGTGTGTACATTGTGCT  
AGATTTAGGTTTTGACCTCAGTCCCAACCAACATTCCATTTGATACCTCGAATGCTTGATCTTC  
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT  
CTGATCCTGAAACAACAAGCTAACGAAGATTACCCAAAAGCCCTTTCTAACCCACAAGAA  
GTTGCGAAGGCTGTATCTGTCCACAATCAACTAAGTGAAATACCACTTAATCTTCCCAAT  
CATTAGCAGAAGCTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAA  
GGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAAACCCTCTTGATAATAATGGGATAGA  
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT  
CAGTTCCTAAGGCTTACCACCACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA  
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCTAGGAAACAA  
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAAATACATT  
TGGAACAATAAACTAAAAAAATCCCTTCAGGATTACCAAGAGTTGAAATAGCTCCAGATA  
ATCTTCTTCACTTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC  
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG  
AATGCAACCTTGCAACATTTCTGTTGTGTTTGAGCAGAATGAGTGTTGAGCTTGGGAACCTT  
GGAATGTAAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAAATCCCTACATT  
TGGAACTACTGAACCTATTAATAATGGTAGTATTATATATACAAGCAAAATCTATTTCTCA  
AGTGGTAAGTCCACTGACTTATTTATGACAAGAAATTCACCGGAATTTTGCCAACTATT  
GATACATAAGGGGTTGAGAGAAAACAAGCATCTATTGCAGTTTCTTTTTCGTACAAATGAT  
CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA  
TTTAAACATTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT  
TAGCAAAATTTGTGCTCTTTCACTTTGCTGTGTAGAAAAACAGAAATTAACAAGACAGTAATGT  
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAAT  
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT  
CTTTATGTTTAAACATTAATTTCTTAAATAAAGCCCTTCAGTAAATGTTCAATTACCAACTTGA  
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATATT  
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACCTCGCATTTT  
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTTGTTAGGCTATATAACATTGCCAC  
TTCACCTCAAGGAATATTTTGGAGATCCCTTTGGAAGACCTGCTTGGGAAGAGCCTGGA  
CACTAACAAATCTACACCAAAATGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA  
TATAAATGCTCAGAGTCTTTATGTATTTCTTATTGGCATCAACATATGTAAATCAGAAA  
ACAGGGAATTTTCATTAAAAATATTGGTTTGAAAT

## **FIGURE 2**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR  
SHFPPFDLFPMCPFGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNNKLTKIHPKAPLTTKKLRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ  
KDTFGKMNALHVLEMSANPLDNNGIEPGAPEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLP  
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

### **Signal sequence.**

amino acids 1-15

### **N-glycosylation site.**

amino acids 281-285

### **N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

### **Leucine zipper pattern.**

amino acids 154-176

0 9 5 4 3 0 3 0 3

TTTGTATTTATTAAAACATTTCTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE  
TWHFDDLQQPFVVMRVCVLCACEAPQWGRRTRGPRVSCNLIKPECPTPACGQPRQLPGHCQQT  
CPQERSSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDGHTDFVALLTGPRSQAVAR  
ARVSLRLSSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL  
LRAEQHLHALVTLLTHPSGEVWGPIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE  
SLHFLLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTVQEMD  
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCADALIPVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLLEAAGAEGVRALGAPDTASAAPPVV  
PGLPALAPAKPGGPGRPDPNTCFEQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC  
PPSCPHVPQAPDQCCPVCEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHVPVPP  
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVNVPTDCKQCPVGSAGHPQLGDPMQADG  
PRGCRFAGQWFPESQSWHPVSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCSGSGKESRCCS  
RCTAHRRPPETRTDPELEKEAEGS

### Signal sequence.

amino acids 1-23

### N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

### Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

### N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

### Amidation site.

amino acids 87-91

### Cell attachment sequence.

amino acids 165-168

### Leucine zipper pattern.

amino acids 315-337

## 0974-684X(200603)24:3;1-L

[illegible]

## FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLLGGAGPRGSSLANVPVPAAPLSAPGPCAAQPCRNNGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHHGNCSSSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVFPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFO  
QCSLIDGRSVTPLQASGGLVLLEEMALGNNHFIGFVNDSTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSTCEEQYVGTFCCEYDACQRKPCQNNASCI DANEKQD  
GSNFTCVCLPGYTGBELCQSKIDYCI LDCRNGATCISSSLGFTQCCEGYFGSACEEKVDPC  
ASSPCQNNGT CYVDGVHFTCNCS PGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG  
YHGLYCEEYNECLSA PCLNAAATCRDLVNGYECVCLAEYKGTHCELYKDCANVSLNGATC  
DSDGLNGTCICAPGFTGEECDIDINECDSNPCHHGSCLDQPNGYNCHCPHGWVGANCEIHL  
QWKS GHMAESLTNMPRHSYIIIGALCVAFILMLIILIVGICRISRIEYQGS SRPAYEEFY N  
CRSIDSEFSNNAIASIRHARFGKSRPAMYDVSPYIAYEDYSPDDKPLVTLIKTDL

### Signal sequence.

amino acids 1-28

### Transmembrane domain.

amino acids 641-660

### N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

### Glycosaminoglycan attachment site.

amino acids 320-324

### Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

### N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

### Amidation site.

amino acids 702-706

### Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

### EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTTCAGGCCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT  
AGGAAAAGGAAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCTTCC  
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

09443-08200  
100280-244460

## FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTCAGGCCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

094413.082004



**0606-3496**

GCTGAGTCTGCTGCTCTCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCTTACACCAACGCGAC  
 GCCCCCCCAGAGCCCTCACCACGCTGGGGCGCCCCAGAGCCACACCAATGCCGGGCACCTAC  
 GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT  
 GATGCGGGACTTCCCCTCTGTTGACGGCCACAACGACCTGCCCTGGTCTTAAGGCAGGTTT  
 ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC  
 AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCA  
 GGACCGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT  
 CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
 TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
 CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA  
 GCTCCGCTAAGGGCGTCCACTCCTTCTACAAACACATCAGCGGGCTGACTGACTTTGGTGAG  
 AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
 TGTGGCACGGCGGGCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC  
 GGGGTGTGTGCAACAGTGTCTGGAATGTTCTGTATGACATCTGCAGCTTCTGAAGAAAGAAC  
 GGTGGCGTCGTATGGTGTCTTTGTCCATGGGAGTAATACAGTGCACCCATCAGCCAATGT  
 GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCTATTGGATCAAGTTCATCGGGA  
 TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATA  
 CCGGTCTGTATAGAGGAGTTGCTGAGTCTGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCT  
 TCGTGGAAACCTGCTCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
 AAAGCCCCTTGGAGGACAAGTTCGCGGATGAGCAGCTGAGCAGTTCTCTGCCACTCCGACCTC  
 TCAGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATA  
 CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCA  
 TCCTTGCAGTGTGTGGCCACCTTCCCAGTCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC  
 TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAGTTCCCTGTGTGTGCAGGCACA  
 AATATTTCTGAAATAAATGTTTTGGACATAG

## FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNLDPLVLRQVYQKGLQDVNLRNFSYG  
QTS�DRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNKGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDAGKFPQGLE  
DVSTYPLVIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEEKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

### **N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

### **N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

### **Renal dipeptidase active site.**

amino acids 134-157

## FIGURE 11

AAAACCTATAAATATTCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
 CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA  
 CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC  
 AACGACCTGCCCTTGGTCTTAAGGCAGGTTTACCAGAAAAGGGCTACAGGATGTTAACTGCG  
 CAATTTAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT  
 TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
 CAGATTGACCTCATACGCCCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
 TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCCTCATCGGTGTAGAGGGTGGCCACTCGC  
 TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC  
 ACCCACACCTGCAACACACCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA  
 CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA  
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCAGCGCGGGCCCTGGAAGTGTACAG  
 GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC  
 TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCCATGG  
 GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC  
 AAGGCTGTCTATGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
 CCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGTGAGTCGTG  
 GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCTGTGGAACCTGCTGCGGGTCTTCAGACAA  
 GTGAAAAGGTACAGGAAGAAAAAAATGGCAAAGCCCTTGGAGGACAAGTTCCTCGGATGA  
 GCAGCTGAGCAGTTCTTCCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT  
 CAGGCCAGGAACCTCACTGAGATTTCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
 GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCACGACCTGA  
 ACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACC

## FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQPWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNLISILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVLSMGVVICNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
```

100230-2744650

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

[illegible]

## FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG  
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDVSNQTSCLAGLKP GTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPSGVPVRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

### Signal sequence.

amino acids 1-30

### Transmembrane domain.

amino acids 44-61

### N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

### N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

### Amidation site.

amino acids 3-7, 79-83, 411-415

### Growth factor and cytokines receptors family signature 2.

amino acids 325-331

0365-0365

[illegible]

## **FIGURE 16**

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKGGLGAKVHTFVVDSCNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

### **Signal sequence.**

amino acids 1-19

### **Transmembrane domain.**

amino acids 170-187

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

### **N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216



# FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGAGCCGGCAGGGAGCGAACCAGGACTG  
 GGGTGACGGCAGGGCAGGGGGCGCTGGCCGGGGAGAAGCGCGGGGGTGGAGCACCACCAA  
 CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT  
 GCGAGAGGACCCCGCGTCCGGGCTCCGGTGCCAGCGCTTATGAGGCCACTCCTCGTCCTGCG  
 TGCTCCTGGGCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCAGCCTCTGCG  
 CCGGGGCACCCCGGCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG  
 CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCAGGGCGGGGA  
 GGCCGGGACTGCCGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGG  
 CCCACCGGGCTGCCGGGAGTGCTCGGTGCCCTCCGCGATCCGCTTCAGCGCCAAGCGCTC  
 CGAGAGCCGGGTGCCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG  
 AGCAGGGACATTACGACGCCGTCAACGGCAAGTTACCTGCCAGGTGCCTGGGGTCTACTAC  
 TTCGCCGTCCATGCCACCGTCTACCGGGCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA  
 ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGG  
 GGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTTGGGTGCAGGTGGGTGTGGGTGACTAC  
 ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTTCTGGTGTAATCCGA  
 CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC  
 TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTTGGGAATATT  
 GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGCTCTGCTGCTGGCAAGGAATGGGAAC  
 AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCAAGACCA  
 GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCCACGGT  
 GGGGTGCTCTCTTCTGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGCTCTCTGGG  
 GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCCTCATAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLLGLAAGSPPLDDNKIPSLCPGHPLPGTPGHHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGRPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP  
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

### **Signal sequence.**

amino acids 1-15

### **N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

### **Cell attachment sequence.**

amino acids 77-80

## FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA  
GCCCTTGGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCCAGGGCTTGGCGTCTTTGTTGAAGTGGTCAG  
CCTATGTTTTCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCTACTCCCCGGAGGCCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCTGCTGTCTGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGAGCTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC  
ACGGCCGGTTCCGGGAGGAGGAGTGTCTGTCGCTCTGTGACATCGGCTACGGGGGAGCCAG  
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT  
CACCTACAAGACCGCCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA  
GTTTTTGCTTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACAGCGCTGC AAAAC  
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCGGTGGGGCCAGGGTCTT  
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA  
CCTTGCACAATGCAGAAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCAGAC  
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

## FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176  
<subunit 1 of 1, 455 aa, 1 stop  
<MW: 50478, pI: 8.44, NX(S/T): 2  
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV  
QPPAADMRRLDWSDSLAAQLAQARAALCGIPTPSLASGLWRTLQVGNWMLLPAGLASFVEVV  
SLWFAEQGRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGG  
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRNLNISTCH  
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGACATKVHFPFHTCDLRIDGDC  
FMVSSEADTYRARMKCQARKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFVIG  
LTYKTAKDSFRWATGEHQAPTSTFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNRQCK  
TRNRYICQFAQEHISRWGPGRS

### Signal sequence.

amino acids 1-26

### Transmembrane domain.

amino acids 110-124

### N-glycosylation sites.

amino acids 144-148, 243-247

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

### N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

### EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

### C-type lectin domain signature.

amino acids 417-442



## FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192  
<subunit 1 of 1, 694 aa, 1 stop  
<MW: 77400, pI: 9.54, NX(S/T): 6  
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRLKTKPLMTEFSVKSTIIS  
RYAFTTVSCRMNLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE  
KRNKTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLP LHN SRQSGSGREDDSGPPSTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRRIKVKDHLISVTPDSIRDGKVYIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNPNYNGSEII IAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDV TG  
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKFPNSVKKKQNKTKKRHRG  
DGVFPLHHLGIR

### Signal sequence.

amino acids 1-14

### N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

### Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

### N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC  
GGCAGCGGCGGCGGCGGCGCTCCCGGGCTCCGGCTTCTGCTGTGTCTTTCTCCGCCGCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACGCTACTGAA  
TCCCAACAGGCAGACCATTATTTTCAAGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTTTCTAGCAGTGAACTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA  
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA  
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCCCTGCGGTCACTGGAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGACATTGAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCAATAACCTAAACAAA  
ACAGATAATGGTACATACCCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCCAACAACACCACCACCA  
CCACCACCACCACCACCACCATCCTTACCATCATCAGATTTCCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCTGGCGGTGGTGGTGTTCGCCAT  
GCTGTGCTTGCTCATCTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

090464-2

&lt;MW: 48240, pI: 4.93, NX(S/T): 7

amino acids 1-36

amino acids 372-393

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

amino acids 233-240, 319-328

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432



## FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA  
 CCGCCAGGAAAGACTGAGGCCGCGGCTGCCCGCCGGCTCCTGCGCGCCGCGCGCTC  
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGTGCTCCTGCTACTGGCCCT  
 GGGGCTGGGGTGCAGGGTGCCTCATCCGGCTGCCAGTGACGCGAGCCACAGACAGTCTTCT  
 GCATGTCCCGCCGAGGGGACACGGTGCCTCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC  
 GTCTTTGAGAACGGCATCACCATGTCTCGACGCAAGCAGCTTTGCCGGCTGCCGGGCTGCA  
 GCTCTGGACCTGTACAGAACAGATGCCAGCTGCGCCTGCCCGCCTGTGTGCTGG  
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG  
 GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGG  
 CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
 GCCTCCGGGGCTGACGCGCTGCGGTGGCCGGCAACACCCGATTGCCAGCTGCGGGCC  
 GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
 CCTGCCTGGCGACCTCTCGGGCTCTTCCCCCGCTGCGGTGCTGGCAGCTGCCCGCAACC  
 CCTTCAACTCGCTGTGCCCTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCA  
 CTGGCCAGCCCTGAGGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT  
 GGAGCTTGACTACGCGACTTTTGCTGCCAGCCACCAACAGCCACGACGATGCCACCA  
 CGAGGCCCGTGGTGCAGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC  
 CCCACAGCGCCGCGCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCC  
 TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG  
 GGACACGCGACCACTTGGCGTGTCTGTGCCCGAAGGCTTACAGGGCTGTACTGTGAGAGC  
 CAGATGGGGCAGGGGACAGGCCCGAGCCCTACACCAAGTACGCGCGAGGCCACACGGTCCCT  
 GACCTGGGCATCGAGCCGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC  
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT  
 AAGCGGCTGGTGACGTGCGACTGCCTGCCTCGCTCGTGAACACGGTCAACCAAGCTGCG  
 GCCCAAGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCAGGAGGCG  
 AGGAGGCTGCGGGGAGGCCATACACCCCGAGCCGTCCACTCCAACCAAGCCCGAGTCAAC  
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATGCGCCCGCCTGGCCGCGGTGCTCCTGGC  
 CGCGTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGGCGGGGCGGGCCATGGCAGCAGCGG  
 CTCAGGACAAAGGGCAGGTGGGGCAGGGGCTGGGCCCTGGAACTGAGGGAGTGAAGTCC  
 CCCTTGGAGCCAGGCCCAAGGCAACAGAGGGCGGTGGAGAGGCCTGCCAGCGGTCTGA  
 GTGTGAGGTGCCACTCATGGGCTTCCAGGGGCTGGCCTCCAGTCAACCCCTCCACGCAAAGC  
 CTTACATTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGCG  
 CAGCCCCCTCTGCTGCCACACCAGTAAAGTTCTCAGTCCCAACCTCGGGGATGTGTGAGA  
 CAGGGCTGTGTGACCACTGAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT  
 CCGCCCTGCCCTCCGCAACGTGCACTCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
 GCATGCTGGGCCCTGCTGGGCTCTCCCACTCCAGCGGACCTTGGGGGCCAGTGAGGAAG  
 CTCGCCGAAAGAGCAGAGGGAGAGCGGCTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG  
 AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA  
 AATATATATATATTTATAAGATCCTTTCCTATTATTCTGGGAAGATGTTTTTCAAATC  
 AGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCTTTTGTAGAAAAA  
 ATAAAAAAAAAA

## FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLL LLL LLL LALGPGVQGCPSGCQCSQFQT V FCTARQGTTPRDPVPD TVGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNIASRLRPRLLLDL SHNSLLALEPGILD TANVEALRL  
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVFPVIRGLRGLTRRLLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPFNCVCPLSWFGPWPVRESHVTLASP  
EETRCHFFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGTRHHLACLCEGFTGLYCESQMGO  
GTRPSPTPVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGS SVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAGVGAAYCVRGRAMAAAAQDKGVGPAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFPGLQSPLHAKPYI

**Signal sequence.**

amino acids 1-23

**Transmembrane domain.**

amino acids 501-522

**N-glycosylation sites.**

amino acids 198-202, 425-429, 453-457

**Tyrosine kinase phosphorylation site.**

amino acids 262-270

**N-myristoylation sites.**

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**EGF-like domain cysteine pattern signature.**

amino acids 355-367

**Leucine zipper pattern.**

amino acids 122-144, 194-216

## FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCGTACCCTTACCCGCCCCGCCACC  
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCCATGCCAGCCTC  
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC  
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGACAGGAGGCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCCATTAACGCCACCTCCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC  
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC  
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCCTACAACAGCT  
GCTATAGCGCAGGTGTCTTCATTACACCAAGGGGATATTCTGAGTGTATAATTCCCCGG  
GCAAGGGCGAAACTTAACTCTCTCCACATGGAACCTTCTCGGGTTTGTGAAACTGTGATT  
GTGTTATAAAAAAGTGGCTCCAGCTTGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC  
CCCGTTCTCACTTTTCCCTTTTCATTCCCACCCCCTAGACTTTGATTTTACGGATATCTTG  
CTTCTGTTCCCATGGAGCTCCG

## FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLAPKGGPPGNMGGFVREPALSVALWLSWGAALGAVACAMALLTQQTTELQSLRREV  
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRRAVLTKQKQKQHSVLHLVPIN  
ATSKDDSDVTEVMWQPALRRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFMTGQVVSREG  
QGRQETLFRICRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRRAKLNLSPHGTFLGFVKL

### Signal sequence.

amino acids 1-40

### N-glycosylation site.

amino acids 124-128

### Tyrosine kinase phosphorylation site.

amino acids 156-164

### N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

## FIGURE 29

CACTTTCTCCCTCTCTTCTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCGAGAGAC  
 CTCGGAGACCGCGCGGGGAGACGAGGCTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA  
 CCGCCCCCACCCTCTCTTCTGCACTGCCGTCTCCGGGAAGACCTTTTCCCTGCTCTGTT  
 TCCTTACCGAGTCTGTGCATCGCCCCGGAACCTGGCCGGGAGGAGGCTTGGCCGGCGGGGAGA  
 TGCTCTAGGGGCGGCGGGGAGAGCGGCGGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC  
 TCCCGTGGACAGGACTCTTGTGCGCTACTGCGCTGCTCCTTGCCTTGTCCCTCTGCGCTGGT  
 CCTGAGTCTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC  
 CGTCGCTCCGGACCATGCGGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCACTCAG  
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC  
 GGCAGCCGCGCTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG  
 ATCGAGGCTCCAAGGGAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGCCACACTGGA  
 CCCAAAGGGCAGAAGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
 CTTTTCGGTGGGCGGGAAGAAGCCCATGCACAGCAACCCTACTACCAGACGGTGATCTTCG  
 ACACGAGTTCGTGAACCTTACGACCACTTCAACATGTTACCGGCAAGTTCCTACTGCTAC  
 GTGCCCGGCTCTACTTCTTCCAGCTCAACGTGCACACCTTGAACCCAGAAGGAGACCTACCT  
 GCACATCATGAAGAACGAGGAGGAGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA  
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCCTC  
 TACAAGGCGCAACGTGAGAACGCCATCTTACGCGAGGAGCTGGACACCTACATCACTTCCAG  
 TGGCTACTGTGTCAAGCACGCCACCGAGCCCTAGCTGCGCGGCCCTCTTCTCTCGGC  
 ACCTTCCACCCTGCGCTGTGCTGACCCACCGCTCTTCCCGCATCCCTGGAATCCGACTC  
 CCTGGCTTTGGCATTCACTGAGAGCGCCTGCACACAGAAAGCCAAAGCGATCGGTGCTCC  
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGACCCCGC  
 GAGAACCCTCTGGGACCTCTCGCGGCCCTCTCTGCACACATCTTCAAGTGAACCCGACGGC  
 GAGACGCGGTGGCGGCAGGGCGTCCAGGGTGGCGCACCGCGCTCCAGTCTCTGGAAATA  
 ATTAGGCAAAATCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
 TTGTTATTTTTGTCTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCTTTTCACTTGAG  
 ACTCTGCTTAAGAGAAGATCAAAGTTAAAGCTCTGGGTGAGGGAGGGGCCGGGGCAGG  
 AAACACTCTTGGCTTAATCTTTTAAAGCCAGTAGGAATCTTCTGAGGATAGGTGGACC  
 CTGACATCCCTGTGCGCTTGGCCAAAGGCTCTGCTGGTCTTCTGAGTCAAGCTGCGAGGT  
 GATGGGGCTGGGGCCCCAGGCGTCAGCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
 TCCAGTTGGTGAAGCAGCGCAAGGGCTCTCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA  
 GGCTCGAGATGTTTCTATGAGGGGCGAGCTCTTGGTACATCATGTGTGGCTCTGCTCC  
 ACCCTGTGCCACCCAGAGCGCTGGGGGGTGGTCTCCATGCTGCCACTTGGCATCGGCT  
 TTTCTGTCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT  
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCTCTGTTGGCTAAGCATCACCCTT  
 CCAGCTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCCCATGCCC  
 CATCCAGGCTCTGACCAGTAGCTGAGAGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG  
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCTGTGAGCCTCAGTCTG  
 AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCTGTGAGGATTCACTCTCAGGAGC  
 TGGGTGGCAGGAGAGGCAATAGCCCTGTGGCAATGACAGGACCAGCTGGAGCAGGGTTGCG  
 GTGCTCTCCAGGTGCTCTGCGCCCTGCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC  
 ATAGCCCTCTCCACTCACCCTATGTTGATGCCAGGGCTACTTGTGTACCCGTGGGCC  
 CCCAAACCCCGCTGCGCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAATCTGTC  
 TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGTCTCCTAAGTCCCTCTCTTAAAGAACTT  
 CTGCGGGTCACTCTGAAGCCGAGTTGCTGTGGCGTGGCCGAAGCAGAGCGCCACACTC  
 GCTGCTTAAGCTCCCCGCTCTTTCAGAAACATTAACATCAGAAATTGTTTTCA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234  
><subunit 1 of 1, 281 aa, 1 stop  
><MW: 31743, pI: 6.83, NX(S/T): 1  
MGSRGQGGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP  
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TGPKGQKGSMPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY  
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDERSIMQSQSLMLELREQDQVWV  
RLYKGERENAI FSEELDTYITFSGYLVKHATEP

### **Signal sequence.**

amino acids 1-25

### **N-glycosylation site.**

amino acids 93-97

### **N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### **Amidation site.**

amino acids 150-154

### **Cell attachment sequence.**

amino acids 104-107

## FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTCGCGCGGTCTTCCCGCGG  
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCATCTGTGCAGCCTCTTAAAGCAAATAAGACCAAGGAGGAGATTAT  
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGGAG  
 CTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGCTAGTCAGAATT  
 GCCTCAAAAAGAGCTAGAAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCAACTGCTACCTATTTTCTGTCTCCCAACGAGGAAGCCTGTCCATTGAAACGAGCA  
 AAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC  
 TAGCCCATCATCACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACTCGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATACCACCTCGGCTACTCCTCAAGCCCGCCACCCTTCTACCCACCAATGCTTTCAGTGACACC  
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAAATGTTATAAACCTA  
 CTGCACCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTGATAGGCC  
 TCGTCTCTCTGGGTAGAATCCTTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCCAGAAAGCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTTCTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCACCTCCGCTCTC  
 CTGGGTTCAAGCGATTTCTCTCGCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG  
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCTCGGCTCCCAAAGTCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGGAGAAGGAATGAAGTG  
 GGAACCAAATAGGTAATTTTGGGTAATCTGCTCTAAATATTAGCTAAAAACAAAGCTCT  
 ATGTAAAGTAATAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCAGATAAAAATCAAC  
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTTAAAACTTATT  
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTTGTTACTCAA

[illegible]

><subunit 1 of 1, 431 aa, 1 stop

MFFGEGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIrgNEPVYTSTQED  
CINSccSTKNISGDKACNLMIFDTRKTARQPNcyLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEIahLLPENVSALPATVAVASPHtTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTtTTFQAP  
TDSKGSLETIPFTEISNLTlTNGVNYNPTALSMSNVESStMNKTASWEGREASPGSSSQGSV  
PENoyGLPFekWLLIGSLLFGVLFVLIGLVLLGRILSESrLRKRYSRLDYLINGIYVDI

amino acids 1-25

## amino acids 384-405

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

## amino acids 415-419

## amino acids 50-57

## amino acids 4-10, 48-54, 315-321



## FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
GCCTCCTTGTGTGCCTTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGTCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA  
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTTATTGAGAGTGTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAAGTAAAGAAATCAGGAACA  
TGAAATTGAGGTCTAGCTGGGTATTTATTGACGACAAAAGGCTTGGAACTCCCTTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAAGAACGAAGCTGAACACTGCAGGGTCTTGAGTAAAT  
GTGTTCTGTATAAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA  
AATCTGGTACGCAGTATTTTATACCAGTATTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

## **FIGURE 34**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777  
><subunit 1 of 1, 235 aa, 1 stop  
><MW: 25982, pI: 9.09, NX(S/T): 2  
MRPLAGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCI PKERS

### **Signal sequence.**

amino acids 1-20

### **N-glycosylation sites.**

amino acids 120-124, 208-212

### **Glycosaminoglycan attachment site.**

amino acids 80-84

### **N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125